

**CERTIFICATE OF MAILING**

I hereby certify that this correspondence is being deposited with the United States Postal Service as First Class Mail in an envelope addressed to:

"Assistant Commissioner for Patents,  
Washington, D.C. 20231"

on June 15, 2001

JAMES J. FARRELL  
Reg. No. 26,162/  
Attorney for Applicant(s)

06/15/01  
Date of  
Signature

**PATENT**

UNUS #Y2-0136-UNI  
Docket #F3247(C)

**RECEIVED**

JUN 29 2001

TECH CENTER 1600/2900

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Customer No.: 000201  
Applicant: Berry et al.  
Serial No.: 09/737,297  
Filed: December 15, 2000  
For: PROCESSES AND ORGANISM FOR THE PRODUCTION OF ANTI-FREEZE  
PROTEINS AND ANTI-FREEZE PROTEIN OBTAINED

Group: 1633  
Edgewater, New Jersey 07020  
June 15, 2001

**RESPONSE**

Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

In response to the Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures, applicants have prepared a sequence listing in paper and computer readable form together with a statement that the submission does not include new matter. All are attached hereto along with a request for a two-month extension of time to respond to the comments by July 12, 2001.

Please amend the application as follows:

### **In The Specification:**

Please enter the paper copy of the Sequence Listing into the Specification.

*On page 4, please amend the paragraph beginning on line 8 and ending on line 26 as follows:*

Figure 1 shows the sequence alignment of the 16S rRNA sequence of *Marinomonas protea* (SEQ ID No 1) (Figure 3) to the corresponding sequence of *Marinomonas communis* (SEQ ID No 4);

Figure 2 is a phylogenetic tree comparing *Marinomonas protea* with its closest phylogenetic relatives.

Figure 3 shows the 16S rRNA sequence alignment of isolate 20 (seq ID 2, upper case) to *Marinomonas protea* 16S rRNA (Seq ID 1; lower case) showing 89.4% similarity.

Figure 4 shows the 16S rRNA sequence alignment of isolate 20 (seq ID 2) to its closest phylogenetic relative *Pseudomonas synxantha* (SEQ ID No 5) showing 99.4% similarity.

Figure 5 is a phylogenetic tree based on 16S rRNA sequences comparing Isolate 20 (SEQ ID 2) with its closest relatives. Multiple sequence alignments were created using the Clustal method with a gap penalty of 10.

Figure 6 shows the result of an RI experiment at time= 0 (6A) and at time = 60 minutes (6B).

Figure 7, 8, 9 relate to the Vickers hardness test as described in the example.

## REMARKS

The application as amended now complies with the requirements of 37 C.F.R. §§ 1.821-1.825 including:

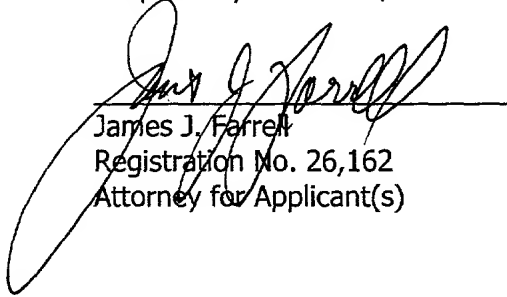
- 1) a computer readable form (CRF) copy of the "sequence listing"
- 2) a paper copy of the "sequence listing" together with an amendment directing its entry into the specification and claims
- 3) a statement that the content of the paper and computer readable copies are the same and include no new matter

Applicants' attorney has been informed by his European colleague that the content of the paper and computer readable copies are the same and include no new matter. Accordingly, based on information and belief, the undersigned believes that the content of the paper and computer readable copies are the same and include no new matter.

Attached hereto is a marked-up version of the changes made to page 4 of the specification. The attachment is captioned "Version With Markings To Show Changes Made".

In view of the foregoing amendments, early favorable action is solicited.

Respectfully submitted,



James J. Farrell  
Registration No. 26,162  
Attorney for Applicant(s)

JJF/lad  
(201) 840-2332

## VERSION WITH MARKINGS TO SHOW CHANGES MADE

### In The Specification:

*On page 4, please amend the paragraph beginning on line 8 and ending on line 26 as follows:*

Figure 1 shows the sequence alignment of the 16S rRNA sequence of *Marinomonas protea* (SEQ ID No 1) (Figure 3) to the corresponding sequence of *Marinomonas communis* (SEQ ID No 4);

Figure 2 is a phylogenetic tree comparing *Marinomonas protea* with its closest phylogenetic relatives.

Figure 3 shows the 16S rRNA sequence alignment of isolate 20 (seq ID 2, upper case) to *Marinomonas protea* 16S rRNA (Seq ID 1; lower case) showing 89.4% similarity.

Figure 4 shows the 16S rRNA sequence alignment of isolate 20 (seq ID 2) to its closest phylogenetic relative *Pseudomonas synxantha* (SEQ ID No 5) showing 99.4% similarity.

Figure 5 is a phylogenetic tree based on 16S rRNA sequences comparing Isolate 20 (SEQ ID 2) with its closest relatives. Multiple sequence alignments were created using the Clustal method with a gap penalty of 10.

Figure 6 shows the result of an RI experiment at time= 0 (6A) and at time = 60 minutes (6B).

Figure 7, 8, 9 relate to the Vickers hardness test as described in the example.